

106001*16812660

Bacillus Subtilis

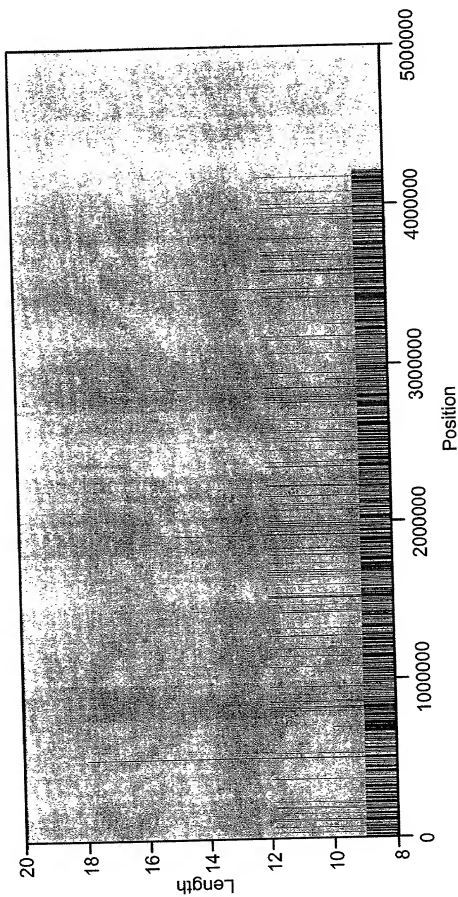


Fig. 1b

1066001' 16817660

Archaeoglobus fulgidus

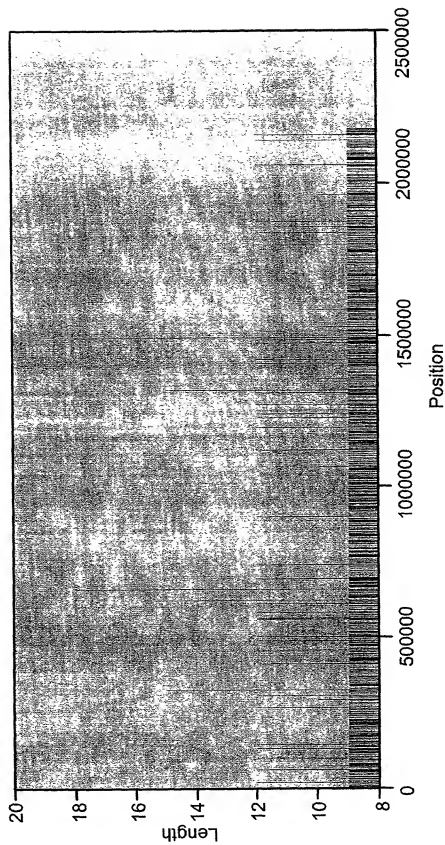


Fig. 1c

106001-108166

Yeast Chromosome 7

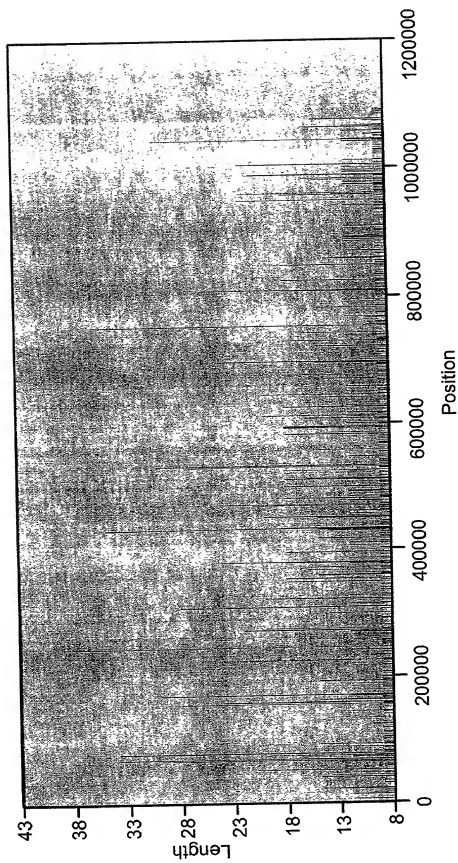


Fig. 1d

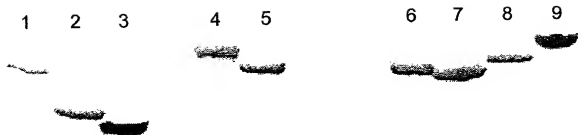


Fig. 2

05971894-100001

1 50

Ec K12, DH5α ---GTTATGT CTTATCCCAC GGTATTTAAT ATGGTTCATT AGGATGTTTA 25*

Ec Bsr9b -TTGTATATGT CTTATCCCAC GGTATTTAAT ATAGTTCATT TGGATGTTCA 26*

Ec Bsr9c TTTGTTATGT CTTATCCCAC GGTATTTAAT ATAGTTCATT TGGATGTTCA 27*

Ec ETEC -TCTATGTTT TATCNCAC GGTNTTTAAT ATGGTTCATT AGGATGTTTA 28*

Consensus -----T-T-- -T---CCCAC GGTATTTAAT AT-GTTCATT -GGATGTT-A 29*

51 100

Ec K12, DH5α TTTCTTGATT TTGCATATGA GTATATTA.. CCCCCCCTC AAAAAAATAA

Ec Bsr9b TTTCTTTATT TTGCATATGA GTATATTA..CCCTT CAAAAAATAA

Ec Bsr9c TTTCTTTATT TTGCATATGA GTATATTA..CCCTT CAAAAAATAA

Ec ETEC TTTCTTGATT TTGCATATGA GTATATTACC CCCCCCCTC AAAAAAATAA

Consensus TTTCTT-ATT TTGCATATGA GTATATTA-- ----CCCT- -AAAAAATAA

101 150

Ec K12, DH5α ATTAATTAAA ATGATGGCTT ATATAAAATA AAATTTAAAG CAAGGAATCT

Ec Bsr9b ATTAATTAAA ACGATTGCTT ATATAAAACA AAATTTAAAG CAAGGAATCT

Ec Bsr9c ATTAATTAAA ACGATTGCTT ATATAAAACA AAATTTAAAG CAAGGAATCT

Ec ETEC ATTAATTAAA ATGATGGCTT ATATNAAATA NAATTTAAAG CAAGGANTCT

Consensus ATTAATTAAA A-GAT-GCTT ATATAAAA-A AAATTTAAAG CAAGGAATCT

151 200

Ec K12, DH5α CAATGGATGT TAAACAAAAT GAGATTTTGT GAAAGCAATA AATTATTGAC

Ec Bsr9b CAATGGATGT TAAACAAAAT GAGATTTAGT GAAACAAATA AATTATTGAC

Ec Bsr9c CAATGGATGT TAAACAAAAT GAGATTTAGT GAAACAAATA AATTATTGAC

Ec ETEC CAATGGATGT TAAACANAAT GAGATTTTGT GAANGCNATN NATTATTGNC

Consensus CAATGGATGT TAAACAAAAT GAGATTTT-GT GAAA-CAATA AATTATT-AC

201 250

Ec K12, DH5α TTCGTTTTAG ATTTGTTTAG CTATAATGTT ATACATTCAA ATGACTGAAC

Ec Bsr9b TTCGTTTTAG ATTTGTTTAG CTATAATGTT ATACATTCAA ATGACTGAAC

Ec Bsr9c TTCGTTTTAG ATTTGTTTAG CTATAATGTT ATACATTCAA ATGACTGAAC

Ec ETEC TTCGTTGTAN ATTTGCTNAG CTATAATGTT ATNCAATTCAA ATGACTGAAC

Consensus TTCGTT- TAG ATTTG-TTAG CTATAATGTT ATACATTCAA ATGACTGAAC

251 264

Ec K12 DH5α ATCCTGTAAT TAAA

Ec Bsr9b ATCCTGTATT TAA-

Ec Bsr9c ATCCTGTAAT TAA-

Ec ETEC ATCCTGTNNT TANA

Consensus ATCCTGTAAT TAA-

* SEQ ID NO

Fig. 3a

1 50
 Ec K12, DH5α TTNNCCCGGA AAAAAATAGG AAAGGGGGGG GGGCTAATCG GCAGGGAAGG 30*
 Ec K12, w3110 TTTNNNCCGG AAAAAATNG AAAGGGGGGG GGGCTAATCG GCAGGGAAGG 31*
 Ec Bsr9c --TTNNCCGG AAAAAATNG AAA..GGGGG GGGCTAATCG GCAGGGAAGG 32*
 Ec (wt) 1 --TTNNCCGA AAAAAANAGG AAAGGGGGGG GGGCTAATCG GCAGGGAAGG 33*
 Ec (wt) 54 -----NCG GAAAAAATG AAA..GGGGG GGGCTAATCG GCAGGGAAGG 34*
 Ec (wt) 68 -----CG GAAAAAATG AAA..GGGGG GGGCTAATCG GCAGGGAAGG 35*

Consensus ----- -AAAAA--G AAA--GGGGG GGGCTAATCG GCAGGGAAGG 36*

51 100
 Ec K12, DH5α CCGCCCCGGA TAGCGGGCGG CANAAGGAAT CANAATTTC AGGTCAGACG
 Ec K12, w3110 CCGCCCCGGA TAGCGGGCGG CAGAAGGAAT CAGAATTTC AGGTCAGACG
 Ec Bsr9c CCGCCCCGGA TAGCGGGCGG CAGAAGGAAT CAGAATTTC AGGTCAGATG
 Ec (wt) 1 CCGCCCCGGA TAGCGGGCGG CAGAAGGAAT CAGAATTTC AGGTCAGACG
 Ec (wt) 54 CCGCCCCGGA TAGCGGGCGG CAGAAGGAAT CAGAATTTC AGGTCAGATG
 Ec (wt) 68 CCGCCCCGGA TAGCGGGCGG CAGAAGGAAT CAGAATTTC AGGTCAGATG

Consensus CCGCCCCGGA TAGCGGGCGG CAGAAGGAAT CAGAATTTC AGGTCAGA-G

101 150
 Ec K12, DH5α GGCTGCAAGT TGCAGACCGT TAAATCATC GGNNGGGGTG TCGTACCACA
 Ec K12, w3110 GGCTGCAAGT TGCAGACCGT TAAATCATC GGTGGGGGTG TCGTACCACA
 Ec Bsr9c GGCTGCAAGT TGCAGACCGT TATAATCATC GGTGGGGGTG TCGTACCACA
 Ec (wt) 1 GGCTGCAAGT TGCAGACCGT TAAATCATC GGTGGGGGTG TCGTACCACA
 Ec (wt) 54 GGCTGCAAGT TGCAGACCGT TATAATCATC GGTGGGGGTG TCGTACCACA
 Ec (wt) 68 GGCTGCAAGT TGCAGACCGT TATAATCATC GGTGGGGGTG TCGTACCACA

Consensus GGCTGCAAGT TGCAGACCGT TA-AATCATC GGTGGGGGTG TCGTACCACA

151 180
 Ec K12, DH5α CTTTACCTGC CGTCAGCCCG AGATTAA-GTT -G
 Ec K12, w3110 CTTTACCTGC CGTCAGCCCG AGATTAA-GTT -G
 Ec Bsr9c CTTTACCTGC CGTCAGCCCG AGATTAA-GTT -G
 Ec (wt) 1 CTTTACCTGC CGTCAGCCCG AGATTAAAGTT TGG
 Ec (wt) 54 CTTTACCTGC CGTCAGCCCG AGAT-AAAGTT TGG
 Ec (wt) 68 CTTTACCTGC CGTCAGCCCG AGAT-AAAGTT TGG

Consensus CTTTACCTGC CGTCAGCCCG AGAT-AA-GTT -G

* SEQ ID NO

Fig. 3b

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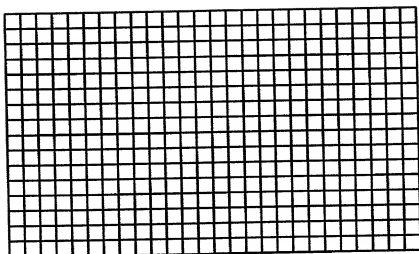


Fig. 4

00071204, 1000001